

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:57:45 ; Search time 27.2445 Seconds

(without alignments)  
1429.075 Million cell updates/sec

Title:	US-09-805-550-2
Perfect score:	2036

Sequence: 1 MKLNKTLKGTNFEIASPD.....EELTANYLLDHGHEFDDQQ 405

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 08

Database : PIR\_73:\*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1187.5	58.3	382	2	T14336	RAD3 protein, iso
2	1127	55.4	392	2	T04150	RAD3 protein, homo
3	925.5	45.5	379	2	T14337	RAD3 protein, iso
4	840.5	41.3	367	2	P96827	Protein F20B17.8 [
5	632	31.0	409	2	S44546	RAD3 protein, homo
6	623	30.6	385	2	CC07783	RAD 23B protein -
7	588	28.9	368	2	T40115	uv excision repair1
8	573	28.1	353	2	S44443	RAD3 protein, homo
9	543	26.7	246	2	G86296	T24018.27 protein
10	483.5	23.7	398	2	S50507	excision repair pr
11	436.5	21.4	372	2	T27774	hypothetical prote
12	361.5	17.8	113	2	H86296	hypothetical prote
13	229.5	11.3	551	2	C84549	F309.1 protein - A
14	211	10.4	536	2	B84549	probable ubiquitin
15	202.5	9.9	542	2	T18562	probable ubiquitin
16	193	9.5	152	2	T51479	hypothetical prote
17	168	8.3	373	2	S54583	hypothetical prote
18	154.5	7.6	354	2	T38404	ubiquitin-like prote
19	154.5	7.6	507	2	T44768	yeast dsk2 homolog
20	150.5	7.4	581	2	T22341	antifreeze glycopo
21	149.5	7.3	1040	2	T29092	hypothetical prote
22	147.5	7.2	424	2	T33663	TSC-22 protein hom
23	147	7.2	252	2	T18584	hypothetical prote
24	146	7.2	681	2	A83455	Fl5c11.2 - Caenorh
25	144.5	7.1	852	2	T46091	DNA polymerase sub
26	144.5	7.1	907	2	AD2951	hypothetical prote
27	144.5	7.1	910	2	H98331	cell division prob
28	144	7.1	638	1	XXAN	divyrolipamide S
29	141.5	6.9	833	2	AF2089	hypothetical prote

30	141.5	6.9	2082	2	T37056	probable multi-domain
31	141	6.9	347	2	H75253	hypothetical protein
32	141	6.9	590	1	T35297	probable dihydrolip
33	141	6.9	639	1	T39141	hypothetical protein
34	140.5	6.9	1167	2	S77213	DNA-directed DNA p
35	140	6.9	638	2	H83690	hypothetical protein
36	140	6.9	2440	2	S38162	transcription coac
37	140	6.9	2441	1	S39161	CREB-binding protea
38	139.5	6.9	1039	2	A12284	translation initiat
39	139.5	6.9	1132	2	A35098	MHC class IIT hist
40	139	6.8	340	2	A35630	regulatory protein
41	138.5	6.8	762	2	H87302	Chemotaxis protein
42	138	6.8	421	2	A60058	neural cell adhesi
43	137.5	6.8	547	2	H83018	dihydrolipoamide a
44	137.5	6.8	865	2	A47282	calcium-binding pr
45	137.5	6.8	873.2	2	A47283	calpoptin - fruit

## ALIGNMENTS

## RESULT 1

T14336

C;Species: *Daucus carota* (carrot)

C:\Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C;Accession: T14336

R; Sturm, A.; Leinhard, S.  
Plant J. 13: 815-821, 1998

Plant J. 13, 813-821, 1993

A/Reference number: 217989; MUID:98345997; PMID:9681019

Accession: T14336

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-382 <STU>

A; Cross-references: **EMB**  
A; Experimental sources:

A; Experimental source: subspecies Queen Anne's Lace, isolate W001C

A:Gene: RAD23-1

C; Superfam

.....  $\mathbf{f}_1, \dots, \mathbf{f}_n$

Query Match	58.38;	Score 1187.5;	DB 2;	Length 382;
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	Matches	255;	Conservative	46;	Mismatches	75;	Indels	31;	Gaps	11.
QY	1	MKLANKITLKGTFEELEASPDASVADYKRIETTGQOSTYRADQOMLITYGKLIKETTILE	60							
Db	1	IKITITLTKSGOFELQVNPDDSVADYKRSIETAGCAAYPAQOMLITYGKLIKGTETLL	60							
QY	61	SGNVAENSLVLMLSKAKASSSGASTATTA---KAPATLAQPAAYVAPASVARTPTQAP	117							
Db	61	ENNAVNESEFIYMLSKSSPSGEGSTTSTAAPKAPQTSAPPSV-APAVS-----QDP	113							
QY	118	VATAEET-AP-PSVQFOAAPATVAATDADYVSOAASNLVFGNNLEQTTQIILDMGGGTW	175							
Db	114	ASTLEVPAPSPAPAPATPATPISAAVGSANVYDASAASILLVAGSNLEGAITQIILDMGGGTW	173							
QY	176	ERDVTYRLRAAYNNPERAIDLYTSGIETENVAQVAYARAPAAQOQTNOQAASPA-QPAVA	234							
Db	174	DRDVTYRLVRAAFNNPERAVERLYTSGIDPEQAAEPAPVSPSG-----QAAVPDQPPAA	228							
QY	235	LPVQSPASAGPNANPLMLFPGVSGSGSNPCVNVGAGSGALDALROLPOFALLQIYOA	294							
Db	229	--AGCAPASAGPNANPLDLFFQGLPDMKSN-----AAGAGNIDFLRTNQOFALRAAYVS	281							
QY	295	NPQILQPMLOELGKNPOILRLIQENQAEFLRLVNESPEGPGGNILGQLAAAVPQTLTV	354							
Db	282	NPQILQPMLOETGKNPNHMLRLIOHQADFLQLINEPMEGGE--NILGH---GQALSTV	335							
QY	355	TPEREATQRLGGMGFNRELYLEVFAACNKKDELTANTLLDHGHEFD	401							
Db	336	TPEEDDATERLEAMGFDERELVEVFAACNKKDELAANTLLDHMHFE	382							

## RESULT 2

T04150

RAD23 protein homolog - rice

C:Species: Oryza sativa (rice)

C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000

C:Accession: T04150

R:Schultz, J.F.; Quatrano, R.S.

Plant Mol. Biol. 34, 557-562, 1997

A:Title: Characterization and expression of a rice RAD23 gene.

A:Reference number: 208695; MUID:97369378; PMID:9225866

A:Accession: T04150

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: EMBL:U63530; NID:g1488296; PIDN:AA65841.1; PID:g1488297

A:Experimental source: cv. Nipponbare

C:Genetics:

A:Gene: RAD23

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 55.4%; Score 1127; DB 2; Length 392;

Best Local Similarity 59.1%; Pred. No. 1.6e-60;

Matches 243; Conservative 48; Mismatches 90; Indels 30; Gaps 9;

QY 1 MKLVNLTGKTNFEIASPDASVADYKRIETTGOSTYRADQOMLIYQGLIKDETTL 60

DB 1 MKLSVTKLKGSTFOIEVDSNOKVADYKRIETTGOGHIYPAEQOMLIHOGKVLKDDTTLD 60

QY 61 SNGVAENFLVIMLSKAKASSGASTATKAPATLAOP--AAPVAPASVARTPTQAPV 118

DB 61 ENKVLNLSFLVIMLSKROKSSS--SAPATSKAPSNQAPPTQVAPAPV-----SOAPV 111

QY 119 ATAETAP-----PSYQAPAPATVATDADYVSOASNLVFGNNLEQTIQOILDMGG 173

DB 112 APATVTPVTVSATPTATASPAPAVAVSSADNVGQATSLVAGSNLEATIOSILEMGG 171

QY 174 THERDTVVALRAVYNNPERADYLSGTPENVEAOPVAPAPAGQOTN--QQAASPAQPA 232

DB 172 IMDRDVTLHALSAFNNPERAVEYLSGVPEQMDI--PV--PPPSIOPAPMPTQASQATQPA 228

QY 233 VALPVQSPASGPNAPNPLIPFGVSGSNPGVPCAGSGGLDLRLQOLPOFALLQV 292

DB 229 A-----PSTLSSGPASPLDLPFPQALPNASTD-----AGGLGLMDLRLNNAQPFRTLLSLV 278

QY 293 QANPOLQELKQNPQILRLIOENQAEFLRLVNESPEGGPGNNIGQLAAVPOTL 352

DB 279 QANPOLQELQELKQNPQILRLIOENQAEFLRLVNESPEGGPGNNIGQLAAVPOTL 352

QY 353 TYPPEREALQRLGEGFNRRLVLEFFPCNKDELTANYLLDGHGHEFDQ 403

DB 339 AVTPEDEALIRLEPMGFDRALVLDVFAFCKNDEQLAANYLLDHMEFADE 389

## RESULT 3

T14337

RAD23 protein, isoform II - carrot

C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T14337

R:Sturm, A.; Leinhardt, S.

Plant J. 13, 815-821, 1998

A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.

A:Reference number: 217989; MUID:98345997; PMID:9681019

A:Accession: T14337

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: EMBL:Y12014; NID:g1914684; PIDN:CAA72742.1; PID:g1914685

A:Experimental source: subspecies Queen Anne's lace, isolate W001C

C:Genetics:

A:Gene: RAD23-2

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

## Query Match

45.5%; Score 925.5; DB 2; Length 379;

Best Local Similarity 50.2%; Pred. No. 1.8e-48;

Matches 203; Conservative 57; Mismatches 117; Indels 27; Gaps 8;

QY 1 MKLVNLTGKTNFEIASPDASVADYKRIETTGOSTYRADQOMLIYQGLIKDETTL 60

DB 1 MKLVNLTGKSHFEIRAPNDYMAIKKNIEDIOGKDNPCGQQLIHNGKVLKDDSTLA 60

QY 61 SNGVAENFLVIMLSKAKA--SSSGASTATTAKAPATLAOPAPVAPASVARTPTQAPV 119

DB 61 ESKISEDGLVYVIMLSKSKMSSTGTTPAQQSSAPATTPAPAPAPAPAPASAVIPT 120

QY 120 TAEFAPPSVQPOQAPATVAAVADADYVSOASNLVFGNNLEQTIQOILDMGGTHERDT 179

DB 121 TVEEAP--LSPAPV-----SDTYGEAASNVVAGSNLEQTIQHIDMGGMMDTNM 169

QY 180 VYRALAAVNNPRAIDYLSGTPENVEA--PYAPAPAGQOTNQQAASPAQVAPV 238

DB 170 VSRALAAVNNPRAVADYLSGTPENVEA--FOGQDINAGNNISDNGV----- 223

QY 239 PSPASGPNAPNPLIPFGVSGSNPGVPCAGSGALDALRLQOLPOFALLQV 298

DB 224 -GAAPAPNSPLNMPPOETLSC-----VTGAGLSLEFLRNPPQFOLRSVQANPOI 276

QY 299 LQPMLELQELKQNPQILRLIOENQAEFLRLVNESPEGGPGNNIGQLAAVPOTLVTPPE 358

DB 277 LQPMLELQELKQNPQILRLIOENQAEFLRLVNESPEGGPGNNIGQLAAVPOTLVTPPE 358

QY 359 REAQLQRLGEGFNRRLVLEFFPCNKDELTANYLLDGHGHEFDQ 402

DB 336 QEAIRLEAMGFDRGLVLEAFIACDRNEELAVYLLLENGDEED 379

## RESULT 4

Protein F20B17.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002

C:Accession: F96827

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96827

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-367 &lt;STO&gt;

A:Cross-references: GB:AE05173; NID:g7715605; PIDN:AA68123.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20B17.8

A:Map position: 1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

## Query Match

41.3%; Score 840.5; DB 2; Length 367;

Best Local Similarity 47.4%; Pred. No. 2.2e-43;

Matches 192; Conservative 53; Mismatches 119; Indels 41; Gaps 8;

QY 1 MKLVNLTGKTNFEIASPDASVADYKRIETTGOSTYRADQOMLIYQGLIKDETTL 60

DB 1 MKLVNLTGSHFEIRVPLSDITMAVKNKINEDSOGKDNPCGQQLIHNGKVLKDDSTLA 60

QY 61 SNGVAENFLVIMLSKAKASSGASTATKAPATLAQAPVAPASVARTPTQAPVAT 120

DB 61 ENKVLNLSFLVIMLSKSKSGS---AGQASVQVCRLLLFHSLFLPLRLSLSTYNPVET 116

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OY 121 AETAPPVQOAPAAVATVATDDADYQSAASLVYNNLEQIOILIDMGGTERDVP 180
Db 117 CSCFTYS-----CSITGTDTIRYQGAASLTYSGSSLEDMVQOIMEMGGSGMDKEY 166
OY 181 VRLALRAAYNNPERAIDLYLSGIDENVE-AQVAPARAPAQOQTNOQASPAQAPALVPQ 239
Db 167 TRLALRAAYNNPERAIDLYLSGIDENVEAQPVEAQAIAQ-----SGAPV-- 211
OY 240 SPASAGNANPDLNFPQGVYSGGSNGVYVAGSAGSLADLRQ-PQFOALLQLOANPQI 298
Db 212 APASAGGNSPSLDLFPQ-----ETVAAGSGDGLGLEPRLRNDDVAITLTISFSIN 262
OY 299 LQPLMLQELGKQNPQILRLIQENQAEFLRLVNESPEGGPG-GNITGLQLAAYPQUTLVTP 357
Db 263 CEPMLQELGKQNPQILRLIQENQAEFLQVNEPYESDSDEGMFDQPEQEMPHATVTPA 322
OY 358 EREALQELGKQNPQILRLVVPFACKNDEFLTANNYLIDGHEHED 402
Db 323 EREALQELGKQNPQILRLVVPFACKNDEFLTANNYLILNLSGDEED 367

```

## RESULT 5

RAD23 protein homolog - human  
N:Alternate names: p58/HHR23B; XP-C repair complementing protein  
C:Species: Homo sapiens (man)  
C:Date: 25-Dec-1994 #sequence\_revision 01-Sep-1995 #text\_change 24-Sep-1999  
C:Accession: S44346  
R:Masutani, C.; Sugawara, K.; Yanagisawa, J.; Sonoyama, T.; Uli, M.; Enomoto, T.; Takio, EMBO J. 13, 1831-1843, 1994  
A:Title: Purification and cloning of a nucleotide excision repair complex involving the  
A:Reference number: S44345; MUID:94222030; PMID:8168482  
A:Accession: S44346  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-409 <MAS>  
A:Cross-references: EMBL:D21090; NTD:g498147; PIDN:BA04652.1; PID:d1005181; PID:g498148  
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology  
C:1-80/Domain: ubiquitin homology <UBH>

Query Match	31.0%	Score 632;	DB 2;	length 409;
Best Local Similarity	34.1%	Pred. NO. 8.1e-31;		
Matches 150;	Conservative 82;	Mismatches 138;	Indels 70;	Gaps 11;

```

0Y      1 M K L V N T L K G N P E I E A S P A S V A D Y K R I I E T T O G S Y R A D O Q M L I Y O G K I L K B E T T L E      60
Db      1 M O V T L K T L Q O O T F I D I D B E T Y K A L K E T I E S E K G D A P P V A G Q K L I Y A G K I L M D T A L K      60
0Y      6 L S N G V A E N S F L V I M L S K A S S G S T A T T K A P A ----- T L A Q P A P V A P A S V      109
Db      6 L E Y K I D E N K F V V V M T K P R A A V S T P R A P A T T Q O S A P A S T T A V T S T T T T V A O A P P V - P A L A P      119
0Y      110 A R P T Q O ----- A V A T A E T A P S P V O Q A P A A T - V A A T O ----- A D V S Q      149
Db      120 T S T A S T I P P A S A T A S S P A S A K O E K P A E T P V A T S P R A T U S T G S D S S R N F E D      179
0Y      150 A A S N L V E G N N L E Q T I O Q I L M G G T W E R D V V A L A A Y N N P E R A I D Y T S G I P E N V E A Q      209
Db      180 A T S A L Y T G O S T E N N Y T E I M S G --- Y E R E V Y I A L R A S F N N P R A E Y I L M G I P G D R E S Q      236
0Y      210 P V A R A P A G O O T N O Q A S P A P A V A L P V O P S P A S P N A N P L N L P Q G V P S G S N P G V V P      269
Db      237 A V U D P P Q A A ----- S T A P O S S A V A A A A A T T T T Y T T ----- T T T S S G A P -----      275
0Y      270 G A G S G A L D A L R O L P O F O A L I Q L V O A N P O I L Q P M I O E I G K O N P O I L R L I O E N Q A E F L R V N      329
Db      276 ----- L E F L N G N Q O F O Q M Q I I O Q N S L P A L L O Q I G R E N P O L D O I G O H Q E H F I O M L N      329
0Y      330 E ----- S P E G P P G N I L G O L A A A V --- O T L V T P P E E R A I O R L E M G E N R E L V L E V P A      381
Db      330 E P V O E A G G O G G G G G G G G I A B A G S G M N Y I O Y T P Q R K A I E R L K A L G P R E G L V I O A Y F A      389
0Y      382 C N K D E L T A N Y L L D H G H E F D      401

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Db      390      | | : | | | : | |      : |
          CEKNENLAANELLQONEDED 409

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## RESULT 6

RAD\_23B protein - channel catfish  
C:Species: *Ictalurus punctatus* (channel catfish)  
C:Date: 02-Apr-2002 #sequence\_revision 02-Apr-2002 #text\_change 02-Apr-2002  
C:Accession: J07783  
R:Lit, Z.; Li, P.; Kocbas, A.; Karsl, A.; Ju, Z.  
Biochem. Biophys. Res. Commun. 289, 317-324, 2001  
A:Title: Microsatellite-containing genes from the channel catfish brain: Evidence of  
A:Reference number: J07783  
A:Contents: Brain  
A:Accession: J07783  
A:Molecule type: mRNA  
A:Residues: 1-585 <Lit>  
C:Comment: This protein with a polythreonine tract, has importance in the nucleotida  
C:Genetics:  
A:Gene: rad23b  
A:Introns: 76/3

Query Match	30.6%	Score 623	DB 2	Length 385
Best Local Similarity	34.6%	Pred. No. 2.6e-30		
Matches 147; Conservative	85;	Mismatches 129;	Indels 64;	Gaps 11

[illegible]

## RESULT 7

uv excision repair protein rad23 homolog - fission yeast (*Schizosaccharomyces pombe*)  
C.Species: *Schizosaccharomyces pombe*  
C.Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #ext\_change 02-Sep-2000  
C.Accession: T40115: T51298  
R.Wood, V. Ralandream, M.A. Barrell, B.G. Taylor, K. Harris, D.  
submitted to the EMBL Data Library, September 1998  
A.Reference number: Z21906  
A.Accession: T40115  
A.Status: Preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 1-368 <MOO>





Db 228 ---LCPEONIDN-----VDEGNDLNLAMPOLAEITATLQONPEMLA 269  
QY 301 PMLDELGNONPILRLIOENQAEFLRLVNESPGGNGILQOLAAVPOQLT----- 353  
Db 270 AVLQGLAAVNPRLVQTIQNNQCAFMDLLNGAGGA-----GAAGNAPERTPPRRHYH 323  
QY 354 VTPEREALQRLGNGFN--RELVLVEFFACKDEELTANLYLDH 396  
Db 324 LSPERAAAIERIKATVNAPEAVVEAYFACDKNEAIAINFISN 368

RESULT 12  
H86296  
F309.1 protein - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 27-Nov-2001  
C:Accession: H86296  
R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzilli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H86296  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-113 <STO>  
A:Cross-references: GB:AE005172; NID:94966345; PIDN:AAD34676.1; GSPDB:GN00141  
A:Genetics:  
A:Map position: 1

Query Match 17.88; Score 361.5; DB 2; Length 113;  
Best Local Similarity 61.18; Pred. No. 2.9e-15;  
Matches 69; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

QY 291 LVQANPQILQMLQELGNQPOLRLIOENQAEFLRLVNESPGGNGILQOLAAV 349  
Db 1 MVNSNPQILQMLQELGNQPOLRLIOENQAEFLRLVNESPGGNGILQOLAAV 349

QY 350 QTLVTPEREALQRLGNGFNRELVLVEFFACKDEELTANLYLDHGHEDD 402  
Db 61 HSNVTPEREALQRLGNGFNRELVLVEFFACKDEELTANLYLDHGHEDD 113

RESULT 13  
C84549  
Probable ubiquitin-like protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: C84549  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: C84549  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-551 <STO>  
A:Cross-references: GB:AE002093; NID:94584343; PIDN:AAD25138.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17200  
A:Map position: 2

Query Match 11.3%; Score 229.5; DB 2; Length 551;  
Best Local Similarity 23.7%; Pred. No. 1.6e-06;

Matches 132; Conservative 61; Mismatches 170; Indels 193; Gaps 26;

QY 3 INVKTLLKGTNFEIEASPDASVADVRRIETTGOSTYRADQOMLIYOGKILKDETTLESN 62  
Db 20 VNIKRSNGTKFVKTSIDSTVESFKEIYAQS--SDVPANQRLIKKGIILKDDQDTLLSY 76  
QY 63 GVAENSLVYIMLSKAKASSGASTATTAKAPATLQAPAPAPASVARTPQAFVATAE 122  
Db 77 GIQADH--TIHWVRSAPSS-----APPAPASQTTAPSVTRGVGSD 117  
QY 123 TA-----PPSVQAPAPATVAATDDADY 147  
Db 118 NSSNLGASPGESLPGLGFNPLGGNMSGFLGAGLPDVLVTOQQLQONPMITDM--IN 176  
QY 148 SQASNLVFGNNLE-----QTIOQLDMG--GGTWERDVTYVRLRAVNPPE-- 192  
Db 177 TPAIQNLNLM--NNPERMSIMNNPQMRRELVDNPELGHVLDNPSTLRQTLKARNPBLMR 234  
QY 193 ---RAIDVLYSGIP-----ENVEAQVAPAPAGQQTNOQASPAQPAV-- 233  
Db 235 EMKRTTDRAMSNIESMPREGFNMLRMYENVQEPFLNNATTMSGNAGNNTGSNPFALLGNQ 294  
QY 234 ALPVPSPAS-----AG--PNANPLNLPPOGVPSG-----GSNPGV-- 267  
Db 235 GYTTGSGDASNNSTPNAQTGTTPANPLP--NPKATGGQTTPARTVNGDANSFGLG 353  
QY 268 VPAGS-----GA-----LDALRQLPQALQVQANPQI-----L 299  
Db 354 IGGTSLGIGLGLGMLGADSPGLGATPPDASQSLQLQNPALISQMGSVSNQYNNQMLSL 413  
QY 300 QPMLQELGNQPOLRLIOENQAEFLRLVNESPE----- 333  
Db 414 NPQLRSMDSNPQLEMMQ--NPDLRQFS--SPEMMQOMTLODSLSONRNTASODAGQT 470  
QY 334 ---GGPG-----NILQOLAA--AVPQTLVTPEREAL--IQLRGMGF--NRELVLVEV 378  
Db 471 GATGNNNGGLDILMMFSLGAGLSTGNQSVNPEERATQLODLQEMGFDRANETRA 530  
QY 379 FFACNKDEELTANLYLL 394  
Db 531 LLATNGNVNAVERLL 546

RESULT 14  
B84549  
Probable ubiquitin-like protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: B84549  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: B84549  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-536 <STO>  
A:Cross-references: GB:AE002093; NID:94584342; PIDN:AAD25137.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17190  
A:Map position: 2

Query Match 10.4%; Score 211; DB 2; Length 536;  
Best Local Similarity 21.5%; Pred. No. 2e-05;  
Matches 125; Conservative 56; Mismatches 142; Indels 258; Gaps 23;

QY 3 INVKTLLKGTNFEIEASPDASVADVRRIETTGOSTYRADQOMLIYOGKILKDETTLESN 62  
Db 20 VNIKRSNGTKFVKTSIDSTVESFKEIYAQ--NSDVPANQRLIKKGIILKDDQDTLLSY 76  
QY 63 GVAENSLVYIMLSKAKASSGASTATTAKAPATLQ-----PAAPVAPASVARTPTQAP 117



